

## Sequence Listing

## (1) GENERAL INFORMATION:

## (i) APPLICANT::

- (A) NAME: Max-Planck-Gesellschaft zur Förderung der Wissenschaften e.V.
- (B) STREET:: none
- (C) CITY: Berlin
- (E) COUNTRY: Germany
- (F) ZIP CODE: none

(ii) TITLE OF THE INVENTION: Nucleic acid molecules encoding proteins which impart the adhesion of *Neisseria* cells to human cells

(iii) NUMBER OF SEQUENCES: 4

## (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

## (vi) DATA OF PRIOR APPLICATION:

- (A) APPLICATION NUMBER: DE 19534579.7
- (B) FILING DATE: 18-SEP-1995

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3287 base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

## (vi) IMMEDIATE SOURCE:

- (A) ORGANISM: *Neisseria gonorrhoeae*
- (B) STRAIN: MS11

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: genomic library in pBA
- (B) CLONE(S): H1967/pES25

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:136..447

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:583..1542

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1585..3111

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CGGCGCAAAC	GGCGGACGCT	GCTGTTAGCC	CCGCTTGAAA	CAAATGCCGT	CTGAACGCCA	60	
CTTCAGACGG	CATTTTATA	ATAAGGCCT	GTCCTAGATA	ACTAGGGAAA	TTCAAATTAA	120	
GTAGAATTAA	TCCCT ATG	AGA AAA AGC	CGT CTA AGC	CGG TAT AAA	CAA AAT	171	
	Met Arg	Lys Ser	Arg Leu	Ser Arg	Tyr Lys	Gln Asn	
1	5				10		
AAA CTC ATT	GAA CTG	TTT GTC	GCA GGC	GTA ACT	GCA AGA	ACA GCA GCA	219
Lys Leu Ile	Glu Leu	Phe Val	Ala Gly	Val Thr	Ala Arg	Thr Ala Ala	
15	20			25			
GAG CCT GAC	AGC ATT	GTT TAT	ACG GAT	TGT TAT	CGT CGC	TAT GAT GTC	267
Glu Pro Asp	Ser Ile	Val Tyr	Thr Asp	Cys Tyr	Arg Arg	Tyr Asp Val	
30	35			40			
TTG GAT GCG	GGC GAA	TTT AGC	CAT TTC	CGT ATC	AAT CAC	AGC ACA CAT	315
Leu Asp Ala	Gly Glu	Phe Ser	His Phe	Arg Ile	Asn His	Ser Thr His	
45	50			55		60	
TTT GCC GAA CGA	CAA AAC	CAT ATT	AAT GGA	ATT GGG	AAC TTT	TGG AAC	363
Phe Ala Glu	Arg Gln	Asn His	Ile Asn	Gly Ile	Gly Asn	Phe Trp Asn	
65	70			75			
CGG GCA AAA CGT	CAT TTA	CGC AAG	TTT GAC	GGC ATT	CCC AAA	GAG CAT	411
Arg Ala Lys	Arg His	Leu Arg	Lys Phe	Asp Gly	Ile Pro	Lys Glu His	
80	85			90			
TTT GAG CCG TAT	TTA AAG	GAG TGC	GAA CGG	CGT TTT	TAACAAACAGT		457
Phe Glu Pro	Tyr Leu	Lys Glu	Cys Glu	Arg Arg	Phe		
95	100						
GAGATAAAAG	TTCTTGTCC	ATTTAAAAC	AATTAGTAAA	ATCGAGTTA	TCCTAGTTGT		517
CCAGGACGGC	CCCTAATTAA	TTTACAATT	TGATACAATT	TGTTTTCAT	CAAAGGAGAA		577
AATCT ATG CGG	GCA CGG	CTG CTG	ATA CCT	ATT CTT	TTT TCG	GTT TTT	624
Met Arg Ala	Arg Leu	Leu Ile	Pro Ile	Leu Phe	Ser Val	Phe	
1	5			10			
ATT TTA TCC	GCC TGC	GGG ACA	CTG ACA	GGT ATT	CCA TCG	CAT GGC GGA	672
Ile Leu Ser	Ala Cys	Gly Thr	Leu Thr	Gly Ile	Pro Ser	His Gly Gly	
15	20			25		30	

GGC AAA CGC TTC GCG GTC GAA CAA GAA CTT GTG GCC GCT TCT GCC AGA Gly Lys Arg Phe Ala Val Glu Gln Glu Leu Val Ala Ala Ser Ala Arg 35	40	45	720
GCT GCC GTT AAA GAC ATG GAT TTA CAG GCA TTA CAC GGA CGA AAA GTT Ala Ala Val Lys Asp Met Asp Leu Gln Ala Leu His Gly Arg Lys Val 50	55	60	768
GCA TTG TAC ATT GCA ACT ATG GGC GAC CAA GGT TCA GGC AGT TTG ACA Ala Leu Tyr Ile Ala Thr Met Gly Asp Gln Gly Ser Gly Ser Leu Thr 65	70	75	816
GGG GGT CGC TAC TCC ATT GAT GCA CTG ATT CGC GGC GAA TAC ATA AAC Gly Gly Arg Tyr Ser Ile Asp Ala Leu Ile Arg Gly Glu Tyr Ile Asn 80	85	90	864
AGC CCT GCC GTC CGC ACC GAT TAC ACC TAT CCG CGT TAC GAA ACC ACC Ser Pro Ala Val Arg Thr Asp Tyr Thr Tyr Pro Arg Tyr Glu Thr Thr 95	100	105	912
GCT GAA ACA ACA TCA GGC GGT TTG ACG GGT TTA ACC ACT TCT TTA TCT Ala Glu Thr Thr Ser Gly Gly Leu Thr Gly Leu Thr Thr Ser Leu Ser 115	120	125	960
ACA CTT AAT GCC CCT GCA CTC TCG CGC ACC CAA TCA GAC GGT AGC GGA Thr Leu Asn Ala Pro Ala Leu Ser Arg Thr Gln Ser Asp Gly Ser Gly 130	135	140	1008
AGT AGG AGC AGT CTG GGC TTA AAT ATT GGC GGG ATG GGG GAT TAT CGA Ser Arg Ser Ser Leu Gly Leu Asn Ile Gly Gly Met Gly Asp Tyr Arg 145	150	155	1056
AAT GAA ACC TTG ACG ACC AAC CCG CGC GAC ACT GCC TTT CTT TCC CAC Asn Glu Thr Leu Thr Thr Asn Pro Arg Asp Thr Ala Phe Leu Ser His 160	165	170	1104
TTG GTA CAG ACC GTA TTT TTC CTG CGC GGC ATA GAC GTT GTT TCT CCT Leu Val Gln Thr Val Phe Phe Leu Arg Gly Ile Asp Val Val Ser Pro 175	180	185	1152
GCC AAT GCC GAT ACA GAT GTG TTT ATT AAC ATC GAC GTA TTC GGA ACG Ala Asn Ala Asp Thr Asp Val Phe Ile Asn Ile Asp Val Phe Gly Thr 195	200	205	1200
ATA CGC AAC AGA ACC GAA ATG CAC CTA TAC AAT GCC GAA ACA CTG AAA Ile Arg Asn Arg Thr Glu Met His Leu Tyr Asn Ala Glu Thr Leu Lys 210	215	220	1248
GCC CAA ACA AAA CTG GAA TAT TTC GCA GTA GAC AGA ACC AAT AAA AAA Ala Gln Thr Lys Leu Glu Tyr Phe Ala Val Asp Arg Thr Asn Lys Lys 225	230	235	1296
TTG CTC ATC AAA CCC AAA ACC AAT GCG TTT GAA GCT GCC TAT AAA GAA Leu Leu Ile Lys Pro Lys Thr Asn Ala Phe Glu Ala Ala Tyr Lys Glu 240	245	250	1344

AAT TAC GCA TTG TGG ATG GGG CCG TAT AAA GTA AGC AAA GGA ATC AAA Asn Tyr Ala Leu Trp Met Gly Pro Tyr Lys Val Ser Lys Gly Ile Lys 255	260	265	270	1392
CCG ACG GAA GGA TTA ATG GTC GAT TTC TCC GAT ATC CGG CCA TAC GGC Pro Thr Glu Gly Leu Met Val Asp Phe Ser Asp Ile Arg Pro Tyr Gly 275	280	285		1440
AAT CAT ACG GGT AAC TCC GCC CCA TCC GTA GAG GCT GAT AAC AGT CAT Asn His Thr Gly Asn Ser Ala Pro Ser Val Glu Ala Asp Asn Ser His 290	295	300		1488
GAG GGG TAT GGA TAC AGC GAT GAA GCA GTG CGA CAA CAT AGA CAA GGG Glu Gly Tyr Tyr Ser Asp Glu Ala Val Arg Gln His Arg Gln Gly 305	310	315		1536
CAA CCT TGATTACACAC TGCCATAACC GCTTGCTGCC AAGGAAAACA AA ATG AAT Gln Pro			Met Asn	1590
320			1	
TTG CCT ATT CAA AAA TTC ATG ATG CTG TTT GCA GCG GCA ATA TCG TTG Leu Pro Ile Gln Lys Phe Met Met Leu Phe Ala Ala Ala Ile Ser Leu 5	10	15		1638
CTG CAA ATC CCC ATT AGT CAT GCG AAC GGT TTG GAT GCC CGT TTG CGC Leu Gln Ile Pro Ile Ser His Ala Asn Gly Leu Asp Ala Arg Leu Arg 20	25	30		1686
GAT GAT ATG CAG GCA AAA CAC TAC GAA CCG GGT GGC AAA TAC CAT CTG Asp Asp Met Gln Ala Lys His Tyr Glu Pro Gly Gly Lys Tyr His Leu 35	40	45	50	1734
TTC GGT AAT GCT CGC GGC AGT GTT AAA AAT CGG GTT TGC GCC GTC CAA Phe Gly Asn Ala Arg Gly Ser Val Lys Asn Arg Val Cys Ala Val Gln 55	60	65		1782
ACA TTT GAT GCA ACT GCG GTC GGC CCC ATA CTG CCT ATT ACA CAC GAA Thr Phe Asp Ala Thr Ala Val Gly Pro Ile Leu Pro Ile Thr His Glu 70	75	80		1830
CGG ACA GGG TTT GAA GGC ATT ATC GGT TAT GAA ACC CAT TTT TCA GGA Arg Thr Gly Phe Glu Gly Ile Ile Gly Tyr Glu Thr His Phe Ser Gly 85	90	95		1878
CAC GGA CAC GAA GTA CAC AGT CCG TTC GAT AAT CAT GAT TCA AAA AGC His Gly His Glu Val His Ser Pro Phe Asp Asn His Asp Ser Lys Ser 100	105	110		1926
ACT TCT GAT TTC AGC GGC GGC GTA GAC GGC GGT TTT ACC GTT TAC CAA Thr Ser Asp Phe Ser Gly Gly Val Asp Gly Gly Phe Thr Val Tyr Gln 115	120	125	130	1974
CTT CAT CGG ACA GGG TCG GAA ATA CAT CCC GCA GAC GGA TAT GAC GGG Leu His Arg Thr Gly Ser Glu Ile His Pro Ala Asp Gly Tyr Asp Gly 135	140	145		2022

CCT CAA GGC GGC GGT TAT CCG GAA CCA CAA GGG GCA AGG GAT ATA TAC Pro Gln Gly Gly Gly Tyr Pro Glu Pro Gln Gly Ala Arg Asp Ile Tyr 150	155	160	2070
AGC TAC CAT ATC AAA GGA ACT TCA ACC AAA ACA AAG ATA AAC ACT GTT Ser Tyr His Ile Lys Gly Thr Ser Thr Lys Thr Lys Ile Asn Thr Val 165	170	175	2118
CCG CAA GCC CCT TTT TCA GAC CGC TGG CTA AAA GAA AAT GCC GGT GCC Pro Gln Ala Pro Phe Ser Asp Arg Trp Leu Lys Glu Asn Ala Gly Ala 180	185	190	2166
GCT TCC GGT TTT CTC AGC CGT GCG GAT GAA GCA GGA AAA CTG ATA TGG Ala Ser Gly Phe Leu Ser Arg Ala Asp Glu Ala Gly Lys Leu Ile Trp 195	200	205	2214
GAA AAC GAC CCC GAT AAA AAT TGG CGG GCT AAC CGT ATG GAT GAT ATT Glu Asn Asp Pro Asp Lys Asn Trp Arg Ala Asn Arg Met Asp Asp Ile 215	220	225	2262
CGC GGC ATC GTC CAA GGT GCG GTT AAT CCT TTT TTA ACG GGT TTT CAG Arg Gly Ile Val Gln Gly Ala Val Asn Pro Phe Leu Thr Gly Phe Gln 230	235	240	2310
GGA TTG GGA GTT GGG GCA ATT ACA GAC AGT GCG GTA AGC CCG GTA ACC Gly Leu Gly Val Gly Ala Ile Thr Asp Ser Ala Val Ser Pro Val Thr 245	250	255	2358
TAT GCG GCA GCA CGG AAA ACT TTA CAG GGT ATT CAC AAT TTA GGA AAT Tyr Ala Ala Ala Arg Lys Thr Leu Gln Gly Ile His Asn Leu Gly Asn 260	265	270	2406
TTA AGT CCG GAA GCA CAA CTT GCC GCC GCG AGC CTA TTA CAG GAC AGT Leu Ser Pro Glu Ala Gln Leu Ala Ala Ser Leu Leu Gln Asp Ser 275	280	285	2454
GCC TTT GCG GTA AAA GAC GGC ATC AAT TCC GCC AGA CAA TGG GCT GAT Ala Phe Ala Val Lys Asp Gly Ile Asn Ser Ala Arg Gln Trp Ala Asp 295	300	305	2502
GCC CAT CCG AAT ATA ACA GCA ACA GCC CAA ACT GCC CTT GCC GTA GCA Ala His Pro Asn Ile Thr Ala Thr Ala Gln Thr Ala Leu Ala Val Ala 310	315	320	2550
GAG GCT GCA GGT ACG GTT TGG GGA GGT AAA AAA GTA GAA CTT AAC CCG Glu Ala Ala Gly Thr Val Trp Gly Gly Lys Lys Val Glu Leu Asn Pro 325	330	335	2598
ACC AAA TGG GAT TGG GTT AAA AAT ACC GGC TAT GAA AAA CCT GCT GCC Thr Lys Trp Asp Trp Val Lys Asn Thr Gly Tyr Glu Lys Pro Ala Ala 340	345	350	2646
CGA CCT ATG CAG ACT GTA GAC GGG GAA ATG GCC GGG AAA AAT AAG CCA Arg Pro Met Gln Thr Val Asp Gly Glu Met Ala Gly Lys Asn Lys Pro 355	360	365	2694
		370	

CCG AAA CCA AGT ACG CAG CAA CAC TCT ACA CAC TCT GAT AAC AAT ATC Pro Lys Pro Ser Thr Gln Gln His Ser Thr His Ser Asp Asn Asn Ile 375 380 385	2742
GGC TTA CCT GCC CCA TAT GTT AAA CCT GAT ACA TCT ATT TCT CCG ACA Gly Leu Pro Ala Pro Tyr Val Lys Pro Asp Thr Ser Ile Ser Pro Thr 390 395 400	2790
GGA ACA ATT CAA GAC CGC ATC AGA TGG ACA AAA TCC AAG TTT CCT ACT Gly Thr Ile Gln Asp Arg Ile Arg Trp Thr Lys Ser Lys Phe Pro Thr 405 410 415	2838
GAG AAA TCT TTA AAT GGA CAT TTC AAA GCT CAT GGA AAA GAA TTT GGC Glu Lys Ser Leu Asn Gly His Phe Lys Ala His Gly Lys Glu Phe Gly 420 425 430	2886
GAT ATA ACC ATT GAA GAC TAC CAA AAA ATG GCG TCT GAT TTG TTA TCA Asp Ile Thr Ile Glu Asp Tyr Gln Lys Met Ala Ser Asp Leu Leu Ser 435 440 445 450	2934
AAA CAG ACA TCG GAC AAG ATA TTA GGT TAT CAG ACG GAA CAT AGA CGA Lys Gln Thr Ser Asp Lys Ile Leu Gly Tyr Gln Thr Glu His Arg Arg 455 460 465	2982
GTG CGC TAT GAT ATC AAT AAC AAT ATC TAT GTT TTG GCC AAT CCA AAA Val Arg Tyr Asp Ile Asn Asn Ile Tyr Val Leu Ala Asn Pro Lys 470 475 480	3030
ACA TTC AAA ATC AAA ACA ATG TTT AAA CCA AAC TTA GGA AAG GAG TAT Thr Phe Lys Ile Lys Thr Met Phe Lys Pro Asn Leu Gly Lys Glu Tyr 485 490 495	3078
TAT GAT GGA GAA TTC AAA AAA GAC ATG GGA AAT TGACGGAGAA ATATGGCTAC Tyr Asp Gly Glu Phe Lys Lys Asp Met Gly Asn 500 505	3131
ATTGTCCTGT TTGCGGAACG GAAGTTATGG ACTATGATAT CTGTGACGTT TGTCAGTGGC	3191
AAAATACAGG AGAAACTAAT ATAGATGGTG GTCCTAATGA AATGACACTT GCGGAGGCGA	3251
AAGAAGCTTA CGCAAAAGGC TTACCAATCA GATAAA	3287

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1136 base pairs
- (B) TYPE: Nucleotid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: GenomIC DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(vi) IMMEDIATE SOURCE:

- (A) ORGANISM: Neisseria gonorrhiae

(B) STRAIN: MS11

(ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 135..1094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

AACAAACAGTG AGATAAAAGT TCTTGTCCA TTTTAAACCA ATTAGTAAAA TCGAGTTAT	60
CCTAGTTGTC CAGGACGGCC CCTAATTAT TTACAATTT GATACAATTT GTTTTCATC	120
AAAGGAGAAA ATCT ATG CGG GCA CGG CTG CTG ATA CCT ATT CTT TTT TCG	170
Met Arg Ala Arg Leu Leu Ile Pro Ile Leu Phe Ser	
510 515 520	
GTT TTT ATT TTA TCC GCC TGC GGG ACA CTG ACA GGT ATT CCA TCG CAT	218
Val Phe Ile Leu Ser Ala Cys Gly Thr Leu Thr Gly Ile Pro Ser His	
525 530 535	
GGC GGA GGC AAA CGC TTC GCG GTC GAA CAA GAA CTT GTG GCC GCT TCT	266
Gly Gly Lys Arg Phe Ala Val Glu Gln Glu Leu Val Ala Ala Ser	
540 545 550	
GCC AGA GCT GCC GTT AAA GAC ATG GAT TTA CAG GCA TTA CAC GGA CGA	314
Ala Arg Ala Ala Val Lys Asp Met Asp Leu Gln Ala Leu His Gly Arg	
555 560 565	
AAA GTT GCA TTG TAC ATT GCA ACT ATG GGC GAC CAA GGT TCA GGC AGT	362
Lys Val Ala Leu Tyr Ile Ala Thr Met Gly Asp Gln Gly Ser Gly Ser	
570 575 580 585	
TTG ACA GGG GGT CGC TAC TCC ATT GAT GCA CTG ATT CGC GGC GAA TAC	410
Leu Thr Gly Arg Tyr Ser Ile Asp Ala Leu Ile Arg Gly Glu Tyr	
590 595 600	
ATA AAC AGC CCT GCC GTC CGC ACC GAT TAC ACC TAT CCG CGT TAC GAA	458
Ile Asn Ser Pro Ala Val Arg Thr Asp Tyr Thr Tyr Pro Arg Tyr Glu	
605 610 615	
ACC ACC GCT GAA ACA ACA TCA GGC GGT TTG ACG GGT TTA ACC ACT TCT	506
Thr Thr Ala Glu Thr Ser Gly Gly Leu Thr Gly Leu Thr Thr Ser	
620 625 630	
TTA TCT ACA CTT AAT GCC CCT GCA CTC TCG CGC ACC CAA TCA GAC GGT	554
Leu Ser Thr Leu Asn Ala Pro Ala Leu Ser Arg Thr Gln Ser Asp Gly	
635 640 645	
AGC GGA AGT AGG AGC AGT CTG GGC TTA AAT ATT GGC GGG ATG GGG GAT	602
Ser Gly Ser Arg Ser Ser Leu Gly Leu Asn Ile Gly Gly Met Gly Asp	
650 655 660 665	

TAT CGA AAT GAA ACC TTG ACG ACC AAC CCG CGC GAC ACT GCC TTT CTT	650		
Tyr Arg Asn Glu Thr Leu Thr Thr Asn Pro Arg Asp Thr Ala Phe Leu			
670	675	680	
TCC CAC TTG GTA CAG ACC GTA TTT TTC CTG CGC GGC ATA GAC GTT GTT	698		
Ser His Leu Val Gln Thr Val Phe Phe Leu Arg Gly Ile Asp Val Val			
685	690	695	
TCT CCT GCC AAT GCC GAT ACA GAT GTG TTT ATT AAC ATC GAC GTA TTC	746		
Ser Pro Ala Asn Ala Asp Thr Asp Val Phe Ile Asn Ile Asp Val Phe			
700	705	710	
GGA ACG ATA CGC AAC AGA ACC GAA ATG CAC CTA TAC AAT GCC GAA ACA	794		
Gly Thr Ile Arg Asn Arg Thr Glu Met His Leu Tyr Asn Ala Glu Thr			
715	720	725	
CTG AAA GCC CAA ACA AAA CTG GAA TAT TTC GCA GTA GAC AGA ACC AAT	842		
Leu Lys Ala Gln Thr Lys Leu Glu Tyr Phe Ala Val Asp Arg Thr Asn			
730	735	740	745
AAA AAA TTG CTC ATC AAA CCC AAA ACC AAT GCG TTT GAA GCT GCC TAT	890		
Lys Lys Leu Leu Ile Lys Pro Lys Thr Asn Ala Phe Glu Ala Ala Tyr			
750	755	760	
AAA GAA AAT TAC GCA TTG TGG ATG GGG CCG TAT AAA GTA AGC AAA GGA	938		
Lys Glu Asn Tyr Ala Leu Trp Met Gly Pro Tyr Lys Val Ser Lys Gly			
765	770	775	
ATC AAA CCG ACG GAA GGA TTA ATG GTC GAT TTC TCC GAT ATC CGG CCA	986		
Ile Lys Pro Thr Glu Gly Leu Met Val Asp Phe Ser Asp Ile Arg Pro			
780	785	790	
TAC GGC AAT CAT ACG GGT AAC TCC GCC CCA TCC GTA GAG GCT GAT AAC	1034		
Tyr Gly Asn His Thr Gly Asn Ser Ala Pro Ser Val Glu Ala Asp Asn			
795	800	805	
AGT CAT GAG GGG TAT GGA TAC AGC GAT GAA GCA GTG CGA CAA CAT AGA	1082		
Ser His Glu Gly Tyr Gly Tyr Ser Asp Glu Ala Val Arg Gln His Arg			
810	815	820	825
CAA GGG CAA CCT TGATTCACAC TGCCATAACC GCTTGCTGCC AAGGAAAACA	1134		
Gln Gly Gln Pro			
AA	1136		

## (2) INFORMATION FOR SEQ ID NO: 3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(vi) IMMEDIATE SOURCE:

- (A) ORGANISM: Neisseria gonorrhoeae
- (B) STRAIN: MS11

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 136..447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CGGCGCAAAC	GGCGGACGCT	GCTGTTAGCC	CCGCTTGAAA	CAAATGCCGT	CTGAACGCCA	60
CTTCAGACGG	CATTTTATA	ATAAGGCCT	GTCCTAGATA	ACTAGGGAAA	TTCAAATTAA	120
GTAGAATTAA	TCCCT ATG	AGA AAA AGC	CGT CTA AGC	CGG TAT AAA	CAA AAT	171
	Met Arg	Lys Ser	Arg Leu	Ser Arg	Tyr Lys	Gln Asn
			325		330	
AAA CTC ATT	GAA CTG	TTT GTC	GCA GGC	GTA ACT GCA	AGA ACA GCA GCA	219
Lys Leu Ile	Glu Leu	Phe Val	Ala Gly	Val Thr Ala	Arg Thr Ala Ala	
335	340			345		
GAG CCT GAC	AGC ATT	GTT TAT	ACG GAT	TGT TAT	CGT CGC TAT	267
Glu Pro Asp	Ser Ile	Val Tyr	Thr Asp	Cys Tyr	Arg Arg Tyr Asp	
350	355			360		
TTG GAT GCG	GGC GAA	TTT AGC	CAT TTC	CGT ATC	AAT CAC AGC ACA CAT	315
Leu Asp Ala	Gly Glu	Phe Ser	His Phe	Arg Ile	Asn His Ser Thr His	
365	370			375	380	
TTT GCC GAA CGA	CAA AAC	CAT ATT	AAT GGA	ATT GGG AAC	TTT TGG AAC	363
Phe Ala Glu	Arg Gln	Asn His	Ile Asn	Gly Ile	Gly Asn Phe Trp Asn	
385	390			395		
CGG GCA AAA CGT	CAT TTA	CGC AAG	TTT GAC	GGC ATT CCC	AAA GAG CAT	411
Arg Ala Lys	Arg His	Lys Leu	Arg Lys	Phe Asp	Gly Ile Pro Lys Glu His	
400	405			410		
TTT GAG CCG TAT	TTA AAG GAG	TGC GAA	CGG CGT	TTT TAACAACAGT		457
Phe Glu Pro	Tyr Leu	Lys Glu	Cys Glu	Arg Arg Phe		
415	420					
GAGATAAAAG	TTCTTGTCC	ATTTAAAAC	AATTAGTAAA	ATCGAGTTA	TCCTAGTTGT	517
CCAGGACGGC	CCCTAATTAA	TTTACAATT	TGATACAATT	TGTTTTCAT	CAAAGGGAGAA	577
AATCT						582

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1744 base pairs

- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(vi) IMMEDIATE SOURCE:

- (A) ORGANISM: Neisseria gonorrhoeae
- (B) STRAIN: MS11

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 42..1568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GATTCACACT	53
GCCATAACCG	
CTTGCTGCCA	
AGGAAAACAA	
A	
ATG	
AAT	
TTG	
CCT	
Met	
Asn	
Leu	
Pro	
105	
ATT	101
CAA	
AAA	
TTC	
ATG	
ATG	
CTG	
TTT	
GCA	
GCG	
GCA	
ATA	
TCG	
TTG	
CTG	
CAA	
Ile	
Gln	
Lys	
Phe	
Met	
Leu	
Phe	
Ala	
Ala	
Ala	
Ile	
Ser	
Leu	
Leu	
Gln	
110	
115	
120	
ATC	149
CCC	
ATT	
AGT	
CAT	
GCG	
AAC	
GGT	
TTG	
GAT	
GCC	
CGT	
TTG	
CGC	
GAT	
GAT	
Ile	
Pro	
Ile	
Ser	
His	
Ala	
Asn	
Gly	
Leu	
Asp	
Ala	
Arg	
Leu	
Arg	
Asp	
Asp	
125	
130	
135	
140	
ATG	197
CAG	
GCA	
AAA	
CAC	
TAC	
GAA	
CCG	
GGT	
GGC	
AAA	
TAC	
CAT	
CTG	
TTC	
GGT	
Met	
Gln	
Ala	
Lys	
His	
Tyr	
Glu	
Pro	
Gly	
Gly	
Lys	
Tyr	
His	
Leu	
Phe	
Gly	
145	
150	
155	
AAT	245
GCT	
CGC	
GGC	
AGT	
GTT	
AAA	
AAT	
CGG	
GTT	
TGC	
GCC	
GTC	
CAA	
ACA	
TTT	
Asn	
Ala	
Arg	
Gly	
Ser	
Val	
Lys	
Asn	
Arg	
Val	
Cys	
Ala	
Val	
Gln	
Thr	
Phe	
160	
165	
170	
GAT	293
GCA	
ACT	
GCG	
GTC	
GGC	
CCC	
ATA	
CTG	
CCT	
ATT	
ACA	
CAC	
GAA	
CGG	
ACA	
Asp	
Ala	
Thr	
Ala	
Val	
Gly	
Pro	
Ile	
Leu	
Pro	
Ile	
Thr	
His	
Glu	
Arg	
Thr	
175	
180	
185	
GGG	341
TTT	
GAA	
GGC	
ATT	
ATC	
GGT	
TAT	
GAA	
ACC	
CAT	
TTT	
TCA	
GGA	
CAC	
GGA	
Gly	
Phe	
Glu	
Gly	
Ile	
Ile	
Gly	
Tyr	
Glu	
Thr	
His	
Phe	
Ser	
Gly	
His	
Gly	
190	
195	
200	
CAC	389
GAA	
GTA	
CAC	
AGT	
CCG	
TTC	
GAT	
AAT	
CAT	
GAT	
TCA	
AAA	
AGC	
ACT	
TCT	
His	
Glu	
Val	
His	
Ser	
Pro	
Phe	
Asp	
Asn	
His	
Asp	
Ser	
Lys	
Ser	
Thr	
Ser	
205	
210	
215	
220	
GAT	437
TTC	
AGC	
GGC	
GTC	
GAC	
GGC	
GGT	
TTT	
ACC	
GTT	
TAC	
CAA	
CTT	
CAT	
Asp	
Phe	
Ser	
Gly	
Gly	
Val	
Asp	
Gly	
Gly	
Phe	
Thr	
Val	
Tyr	
Gln	
Leu	
His	
225	
230	
235	
CGG	485
ACA	
GGG	
TCG	
GAA	
ATA	
CAT	
CCC	
GCA	
GAC	
GGA	
TAT	
GAC	
GGG	
CCT	
CAA	
Arg	
Thr	
Gly	
Ser	
Glu	
Ile	
His	
Pro	
Ala	
Asp	
Gly	
Tyr	
Asp	
Gly	
Pro	
Gln	

240	245	250	
GGC GGC GGT TAT CCG GAA CCA CAA GGG GCA AGG GAT ATA TAC AGC TAC Gly Gly Gly Tyr Pro Glu Pro Gln Gly Ala Arg Asp Ile Tyr Ser Tyr 255	260	265	533
CAT ATC AAA GGA ACT TCA ACC AAA ACA AAG ATA AAC ACT GTT CCG CAA His Ile Lys Gly Thr Ser Thr Lys Thr Lys Ile Asn Thr Val Pro Gln 270	275	280	581
GCC CCT TTT TCA GAC CGC TGG CTA AAA GAA AAT GCC GGT GCC GCT TCC Ala Pro Phe Ser Asp Arg Trp Leu Lys Glu Asn Ala Gly Ala Ala Ser 285	290	295	629
GGT TTT CTC AGC CGT GCG GAT GAA GCA GGA AAA CTG ATA TGG GAA AAC Gly Phe Leu Ser Arg Ala Asp Glu Ala Gly Lys Leu Ile Trp Glu Asn 305	310	315	677
GAC CCC GAT AAA AAT TGG CGG GCT AAC CGT ATG GAT GAT ATT CGC GGC Asp Pro Asp Lys Asn Trp Arg Ala Asn Arg Met Asp Asp Ile Arg Gly 320	325	330	725
ATC GTC CAA GGT GCG GTT AAT CCT TTT TTA ACG GGT TTT CAG GGA TTG Ile Val Gln Gly Ala Val Asn Pro Phe Leu Thr Gly Phe Gln Gly Leu 335	340	345	773
GGA GTT GGG GCA ATT ACA GAC AGT GCG GTA AGC CCG GTA ACC TAT GCG Gly Val Gly Ala Ile Thr Asp Ser Ala Val Ser Pro Val Thr Tyr Ala 350	355	360	821
GCA GCA CGG AAA ACT TTA CAG GGT ATT CAC AAT TTA GGA AAT TTA AGT Ala Ala Arg Lys Thr Leu Gln Gly Ile His Asn Leu Gly Asn Leu Ser 365	370	375	869
CCG GAA GCA CAA CTT GCC GCC GCG AGC CTA TTA CAG GAC AGT GCC TTT Pro Glu Ala Gln Leu Ala Ala Ser Leu Leu Gln Asp Ser Ala Phe 385	390	395	917
GCG GTA AAA GAC GGC ATC AAT TCC GCC AGA CAA TGG GCT GAT GCC CAT Ala Val Lys Asp Gly Ile Asn Ser Ala Arg Gln Trp Ala Asp Ala His 400	405	410	965
CCG AAT ATA ACA GCA ACA GCC CAA ACT GCC CTT GCC GTA GCA GAG GCT Pro Asn Ile Thr Ala Thr Ala Gln Thr Ala Leu Ala Val Ala Glu Ala 415	420	425	1013
GCA GGT ACG GTT TGG GGA GGT AAA AAA GTA GAA CTT AAC CCG ACC AAA Ala Gly Thr Val Trp Gly Gly Lys Lys Val Glu Leu Asn Pro Thr Lys 430	435	440	1061

TGG GAT TGG GTT AAA AAT ACC GGC TAT GAA AAA CCT GCT GCC CGA CCT Trp Asp Trp Val Lys Asn Thr Gly Tyr Glu Lys Pro Ala Ala Arg Pro 445 450 455 460	1109
ATG CAG ACT GTA GAC GGG GAA ATG GCC GGG AAA AAT AAG CCA CCG AAA Met Gln Thr Val Asp Gly Glu Met Ala Gly Lys Asn Lys Pro Pro Lys 465 470 475	1157
CCA AGT ACG CAG CAA CAC TCT ACA CAC TCT GAT AAC AAT ATC GGC TTA Pro Ser Thr Gln Gln His Ser Thr His Ser Asp Asn Asn Ile Gly Leu 480 485 490	1205
CCT GCC CCA TAT GTT AAA CCT GAT ACA TCT ATT TCT CCG ACA GGA ACA Pro Ala Pro Tyr Val Lys Pro Asp Thr Ser Ile Ser Pro Thr Gly Thr 495 500 505	1253
ATT CAA GAC CGC ATC AGA TGG ACA AAA TCC AAG TTT CCT ACT GAG AAA Ile Gln Asp Arg Ile Arg Trp Thr Lys Ser Lys Phe Pro Thr Glu Lys 510 515 520	1301
TCT TTA AAT GGA CAT TTC AAA GCT CAT GGA AAA GAA TTT GGC GAT ATA Ser Leu Asn Gly His Phe Lys Ala His Gly Lys Glu Phe Gly Asp Ile 525 530 535 540	1349
ACC ATT GAA GAC TAC CAA AAA ATG GCG TCT GAT TTG TTA TCA AAA CAG Thr Ile Glu Asp Tyr Gln Lys Met Ala Ser Asp Leu Leu Ser Lys Gln 545 550 555	1397
ACA TCG GAC AAG ATA TTA GGT TAT CAG ACG GAA CAT AGA CGA GTG CGC Thr Ser Asp Lys Ile Leu Gly Tyr Gln Thr Glu His Arg Arg Val Arg 560 565 570	1445
TAT GAT ATC AAT AAC AAT ATC TAT GTT TTG GCC AAT CCA AAA ACA TTC Tyr Asp Ile Asn Asn Ile Tyr Val Leu Ala Asn Pro Lys Thr Phe 575 580 585	1493
AAA ATC AAA ACA ATG TTT AAA CCA AAC TTA GGA AAG GAG TAT TAT GAT Lys Ile Lys Thr Met Phe Lys Pro Asn Leu Gly Lys Glu Tyr Tyr Asp 590 595 600	1541
GGA GAA TTC AAA AAA GAC ATG GGA AAT TGACGGAGAA ATATGGCTAC Gly Glu Phe Lys Lys Asp Met Gly Asn 605 610	1588
ATTGTCTGT TTGCGGAAC TGAAGTTATGG ACTATGATAT CTGTGACGTT TGTCAGTGGC	1648
AAAATACAGG AGAAACTAAT ATAGATGGTG GTCCTAATGA AATGACACTT GCGGAGGCCA	1708
AAGAAGCTTA CGCAAAAGGC TTACCAATCA GATAAA	1744